

11420122.APP  
SEQUENCE LISTING

<110> Pausch, Mark H  
Price, Laura A

<120> POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,  
AND METHODS OF USING SAME

<130> 01142.0122 SEQUENCE LISTING

<140> 08/816,011  
<141> 1997-03-11

<150> 07/332,312  
<151> 1994-10-31

<150> PCT/US95/14364  
<151> 1995-10-25

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<170> PatentIn Ver. 2.1

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Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe
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Val	Val	Ile	Ala	Leu	Ile	Pro	Gly	Ile	Ala	Leu	Phe	Leu	Val	Leu	Pro
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Cys	Val	Gly	Val	His	Leu	Leu	Arg	Glu	Leu	Gly	Leu	Ser	Ser	Ile	Ser
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210				215						220					

Val	Pro	Thr	Phe	Gly	Ala	Asn	Gln	Pro	Lys	Glu	Phe	Gly	Gly	Trp	Phe
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Val	Val	Tyr	Gln	Ile	Phe	Val	Ile	Val	Trp	Phe	Ile	Phe	Ser	Leu	Gly
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Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr  
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Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr  
305 310 315 320

Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp  
325 330 335

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Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly  
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Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu  
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Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu  
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Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu  
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Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser  
420 425 430

Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr  
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Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu  
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Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu  
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Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln  
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Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met  
500 505 510

Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His  
515 520 525

Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp  
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Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala  
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Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro  
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Asp Pro Arg Trp Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val  
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Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg  
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Met Ala Ala Trp Pro Ala Ala Ala Gly  
 610                   615

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&lt;213&gt; Caenorhabditis elegans

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&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Caenorhabditis elegans

&lt;400&gt; 4

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Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser  
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Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn  
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Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser  
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Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly  
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Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys  
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Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His  
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Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile  
 115             120             125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val  
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130

135

140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser  
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Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly  
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Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu  
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Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe  
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Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val  
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Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln  
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&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 7

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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 8

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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 10

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&lt;210&gt; 12

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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 12

Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly Tyr Gly Asp  
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&lt;211&gt; 24

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&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 13

Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly Tyr Gly Asp  
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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 14

Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly Tyr Gly Asp  
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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 16

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&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 17

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&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 18

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&lt;213&gt; Drosophila melanogaster

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&lt;213&gt; Drosophila melanogaster

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Leu Met Pro Arg Arg Asp Gly Tyr

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&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

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&lt;213&gt; Drosophila melanogaster

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&lt;212&gt; DNA

&lt;213&gt; Drosophila melanogaster

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&lt;211&gt; 27

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&lt;213&gt; Drosophila melanogaster

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ctttttccatc	cattttcttt	ttttttttttt	tatctgttcc	agacgcgtgc	ttatcctgtt	1080
ttcttttgagt	tttctgtat	ttttttgtt	ggtggaaat	ccatgtttt	ttcacatgg	1140
tacctcagcg	ctctggcaat	gggatatact	ccaaacgtcg	ttgcataatca	ctactcaaga	1200
tttgcgcgtc	agttttccgt	ttgcacttctt	atggttggcc	tttcttccgg	tggcctgtgg	1260
cccgttgtta	ttagcactt	cggtggacaag	ccaaatgtat	tataaaatatt	tatagcattt	1320
gagtatactt	gttataatgtt	tttttttatta	agctgtggaa	taaaataatt	attaaaaaaaa	1380
aaaaaaaaaa						1388

&lt;210&gt; 37

&lt;211&gt; 481

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 37

Met	Ser	Pro	Asn	Arg	Trp	Ile	Leu	Leu	Ile	Phe	Tyr	Ile	Ser	Tyr
1					5			10				15		

Leu	Met	Phe	Gly	Ala	Ala	Ile	Tyr	Tyr	His	Ile	Glu	His	Gly	Glu
						20		25			30			

Lys	Ile	Ser	Arg	Ala	Glu	Gln	Arg	Lys	Ala	Gln	Ile	Ala	Ile	Asn	Glu
						35		40			45				

Tyr	Leu	Leu	Glu	Glu	Leu	Gly	Asp	Lys	Asn	Thr	Thr	Thr	Gln	Asp	Glu
					50		55			60					

Ile	Leu	Gln	Arg	Ile	Ser	Asp	Tyr	Cys	Asp	Lys	Pro	Val	Thr	Leu	Pro
						65		70		75		80			

Pro	Thr	Tyr	Asp	Asp	Thr	Pro	Tyr	Thr	Trp	Thr	Phe	Tyr	His	Ala	Phe
						85		90			95				

Phe	Phe	Ala	Phe	Thr	Val	Cys	Ser	Thr	Val	Gly	Tyr	Gly	Asn	Ile	Ser
					100			105			110				

Pro	Thr	Thr	Phe	Ala	Gly	Arg	Met	Ile	Met	Ile	Ala	Tyr	Ser	Val	Ile

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115 120 125

Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe  
130 135 140Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met  
145 150 155 160Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr  
165 170 175Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro  
180 185 190Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser  
195 200 205Leu Tyr Tyr Ser Tyr Val Thr Ile Thr Thr Ile Gly Phe Gly Asp Tyr  
210 215 220Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe  
225 230 235 240Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly  
245 250 255Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys  
260 265 270Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr  
275 280 285Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg  
290 295 300Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr  
305 310 315 320Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp  
325 330 335Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg  
340 345 350Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly  
355 360 365Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu  
370 375 380Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu  
385 390 395 400Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu  
405 410 415Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser  
420 425 430Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr  
435 440 445Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu  
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450

455

460

Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu  
465 470 475 480

Trp

&lt;210&gt; 38

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Caenorhabditis elegans

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (337)

&lt;223&gt; X AT RESIDUE 337 IS AN UNKNOWN RESIDUE

&lt;400&gt; 38

Met Ser Asp Gln Leu Phe Val Ala Phe Glu Lys Tyr Phe Leu Thr Ser  
1 5 10 15

Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser  
20 25 30

Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn  
35 40 45

Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser  
50 55 60

Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Cys Leu Ala Gly  
65 70 75 80

Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys  
85 90 95

Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His  
100 105 110

Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile  
115 120 125

Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val  
130 135 140

Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser  
145 150 155 160

Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly  
165 170 175

Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu  
180 185 190

Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Gln Lys Phe  
195 200 205

Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val  
210 215 220

Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln  
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11420122.APP  
 225            230            235            240

Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val  
 245            250            255

Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser  
 260            265            270

Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile  
 275            280            285

Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr  
 290            295            300

Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ala Ile Asp Met Gln  
 305            310            315            320

Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys  
 325            330            335

xaa

<210> 39

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DEGENERATE  
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<220>

<221> variation

<222> (2)

<223> N AT BASE 2 INDICATES ANY NUCLEOTIDE

<400> 39

tnggatwygg wgaywyt

17

<210> 40

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DEGENERATE  
PRIMER BASED ON HUMAN POTASSIUM CHANNELS

<400> 40

rtcwccrwah ccdaydgt

18

<210> 41

<211> 28

<212> DNA

<213> Homo sapiens

<400> 41

cgcaggcaga gccacaaaga gtacacag

28

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<210> 42  
<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 42  
ggagatcagc taggcaccat atttgg

26

<210> 43  
<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 43  
atgctgcatt cctcatgttt cccagc

26

<210> 44  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 44  
ggttatttaa agagaggct

20

<210> 45  
<211> 426  
<212> PRT  
<213> Homo sapiens

<400> 45  
Met Leu Pro Ser Ala Ser Arg Glu Arg Pro Gly Tyr Arg Ala Gly Val  
1 5 10 15

Ala Ala Pro Asp Leu Leu Asp Pro Lys Ser Ala Ala Gln Asn Ser Lys  
20 25 30

Pro Arg Leu Ser Phe Ser Thr Lys Pro Thr Val Leu Ala Ser Arg Val  
35 40 45

Glu Ser Asp Thr Thr Ile Asn Val Met Lys Trp Lys Thr Val Ser Thr  
50 55 60

Ile Phe Leu Val Val Val Leu Tyr Leu Ile Ile Gly Ala Thr Val Phe  
65 70 75 80

Lys Ala Leu Glu Gln Pro His Glu Ile Ser Gln Arg Thr Thr Ile Val  
85 90 95

Ile Gln Lys Gln Thr Phe Ile Ser Gln His Ser Cys Val Asn Ser Thr  
100 105 110

Glu Leu Asp Glu Leu Ile Gln Gln Ile Val Ala Ala Ile Asn Ala Gly  
115 120 125

Ile Ile Pro Leu Gly Asn Thr Ser Asn Gln Ile Ser His Trp Asp Leu  
130 135 140

Gly Ser Ser Phe Phe Phe Ala Gly Thr Val Ile Thr Thr Ile Gly Phe  
145 150 155 160

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Gly Asn Ile Ser Pro Arg Thr Glu Gly Gly Lys Ile Phe Cys Ile Ile  
165 170 175

Tyr Ala Leu Leu Gly Ile Pro Leu Phe Gly Phe Leu Leu Ala Gly Val  
180 185 190

Gly Asp Gln Leu Gly Thr Ile Phe Gly Lys Gly Ile Ala Lys Val Glu  
195 200 205

Asp Thr Phe Ile Lys Trp Asn val Ser Gln Thr Lys Ile Arg Ile Ile  
210 215 220

Ser Thr Ile Ile Phe Ile Leu Phe Gly Cys Val Leu Phe Val Ala Leu  
225 230 235 240

Pro Ala Ile Ile Phe Lys His Ile Glu Gly Trp Ser Ala Leu Asp Ala  
245 250 255

Ile Tyr Phe Val Val Ile Thr Leu Thr Thr Ile Gly Phe Gly Asp Tyr  
260 265 270

Val Ala Gly Gly Ser Asp Ile Glu Tyr Leu Asp Phe Tyr Lys Pro Val  
275 280 285

Val Trp Phe Trp Ile Leu Val Gly Leu Ala Tyr Phe Ala Ala Val Leu  
290 295 300

Ser Met Ile Gly Arg Leu Val Arg Val Ile Ser Lys Lys Thr Lys Glu  
305 310 315 320

Glu Val Gly Glu Phe Arg Ala His Ala Ala Glu Trp Thr Ala Asn Val  
325 330 335

Thr Ala Glu Phe Lys Glu Thr Arg Arg Arg Leu Ser Val Glu Ile Tyr  
340 345 350

Asp Lys Phe Gln Arg Ala Thr Ser Ile Lys Arg Lys Leu Ser Ala Glu  
355 360 365

Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Arg Arg Thr Leu  
370 375 380

Ser Val Asn His Leu Thr Ser Glu Arg Asp Val Leu Pro Pro Leu Leu  
385 390 395 400

Lys Thr Glu Ser Ile Tyr Leu Asn Gly Leu Ala Pro His Cys Ala Gly  
405 410 415

Glu Glu Ile Ala Val Ile Glu Asn Ile Lys  
420 425

<210> 46  
<211> 2130  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (35)  
<223> N AT POSITION 35 INDICATES UNDETERMINED  
NUCLEOTIDE

11420122.APP

<220>  
 <221> unsure  
 <222> (2057)  
<223> N AT POSITION 2057 INDICATES UNDETERMINED NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2067)  
<223> N AT POSITION 2067 INDICATES UNDETERMINED NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2111)  
<223> N AT POSITION 2111 INDICATES UNDETERMINED NUCLEOTIDE

<220>  
 <221> unsure  
 <222> (2120)  
<223> N AT POSITION 2120 INDICATES UNDETERMINED NUCLEOTIDE

&lt;400&gt; 46

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cgtcagctc	ggagcgcgca	gccccgtctt	gaataagaag	tgagttacaat	ggcggtgtttg	120
aaaaaaaaag	cttcaagtcc	gtcttttca	aaaaacattt	tgaatgtctgc	atgcctcatg	180
tttccccageg	cctcgccggg	gagaccggc	tatagagcag	gagttggcggc	acctgacttg	240
ctggatccca	aatctgcccgc	tcagaactcc	aaaccggaggc	tctcattttc	cacgaaaccc	300
acagtgcctg	cttcccgggt	ggagagtgc	acgaccattt	atgttatgaa	atggaagacg	360
gtctccacga	tatccctgggt	ggtttgtcc	tatctgatca	tcggagccac	cgtgttcaaa	420
gcattggagc	aggctcatga	gatttcacag	aggaccacca	tttgtatcca	gaagcaaaca	480
ttcatatccc	aacattccctg	tgtcaattcg	acggagctgg	atgaactcat	tcagcaaata	540
gtggcagcaa	taaatgcagg	gattataccg	ttaggaaaca	cctccaaatca	aatcagtcac	600
tgggatttgg	gaagttccctt	cttctttgtt	gcaactgtt	ttacaaccat	aggattttgg	660
aacatctcac	cacgcacaga	aggcgcaaa	atattctgt	tcatctatgc	tttactggga	720
attcccccct	ttgggtttct	tttggctgg	tttggagatc	agctaggcac	catattttgg	780
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cgcacatcat	caacaatcat	atttatacta	tttggctgtt	tacttttgt	ggctctggct	900
gcgatcatat	tcaaacacat	agaaggctgg	agtgcctgg	acgcacattt	tttttgtgtt	960
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gggggaacaa	aatagataca	cccatcatgg	tcatctatca	tcaagagaat	tttggaaattct	1620
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gatcagttct	taacttttca	gggtctacct	aactgagct	agatatggac	cattttatgg	1860
tgacaacaat	tttttttttg	taaatgacaa	aaaattctta	tgcagcctt	tacctaagaa	1920
attttctgtca	gtgccttatac	ttatgaagaa	acagaacctc	tctagctaat	gtgtggttt	1980
tccttccttg	ccccccaccccc	taggctcacc	tctgcagtt	tttacccctag	ttctccctt	2040
tgaataccat	accctgtgtgg	aaacagngtg	taaaatgact	gaagtgtatga	tgccgaaagat	2100
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<210> 47  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 47  
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27

<210> 48  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 48  
aaagtgcacc tatttgatgt tctcaat

27

<210> 49  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 49  
aaaaagctta aaatgcttcc cagcgcc

27

<210> 50  
<211> 27  
<212> DNA  
<213> Homo sapiens

<400> 50  
aaatctagac tatttgatgt tctcaat

27

<210> 51  
<211> 534  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (262)  
<223> N AT POSITION 262 INDICATES UNDETERMINED  
NUCLEOTIDE

<400> 51  
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gaggcaggcc agctagaacc tgggcccggc cagttcaagg ccaccagagg gcagccttct 120  
gcggaaaggca gtattggggtt aggccaggac cccagcagac atggcactca gagctctcac 180  
tgtccactga ctctctcttc tccagggttat ggccacatgg ccccaactatc gcccaggcgga 240  
aggcccttct gcatggtctt antagccctt gggctgccag cctcccttagc tctcgtggcc 300  
accctgcgcc attgcctgct gcctgtgtc agccgccccat gtgcctgggt agcggtccac 360  
tggcagctgt caccggccag ggctgcgcgt ctgcaggcag ttagcactggg actgctggtg 420  
gccagcagct ttgtgcgtct gcccaggcgt gtgcgtgtggg gccttcaggg cgactgcagc 480  
ctgcgtggggg ccgtctactt ctgcgtcagc tcgcgtcagca ccattggcct gggg 534

<210> 52  
<211> 956  
<212> DNA

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&lt;213&gt; MUS musculus

&lt;400&gt; 52

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 acgaggagaa tggcgacgc ttggctcta tcgtgtcac cttcacctac ctgctggtgg 120  
 gceeegeggt gttcgacgca cggagatgg agecgagat gatecgagcgg cagcggctgg 180  
 agctgcggca gctggagctg cgggcgcgct acaacctcag cgaggccgg tacgaggagc 240  
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 gtccttcata cttcgccatc accgtcatca ccaccatcg ctaggtcat gcggcgccca 360  
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 gtggccaaagag ggggcgtggc atgcggcagc cccaaatgttc catggccaac atggtgctca 540  
 tcggtttcgt gtctgtgcata agcacgtgt gcatcgccgc agctgccttc tcctactacg 600  
 agcgctggac tttcttccag gcctattact actgcattcat caccctcacc accatcggt 660  
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 cttcagcttc gtgtacatcc tcacggcctc acggtcatacg gcgttcctc aacctcggt 780  
 tgcgtcgatt catgaccatg aacgccgagg acgagaagcg tgcgtcgagg caccgcggcc 840  
 tgctcacgca caacggccag gctgtcgcc tgggtggct gagctgcctg agcggtagcc 900  
 tgggcgacgg cgtgcgtcccc cgcgaccctag tcacatgcgc tgcggccgca agctta 956

&lt;210&gt; 53

&lt;211&gt; 1055

&lt;212&gt; DNA

&lt;213&gt; MUS musculus

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (247)

&lt;223&gt; N AT POSITION 247 INDICATES UNDETERMINED NUCLEOTIDE

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (593)

&lt;223&gt; N AT POSITION 593 INDICATES UNDETERMINED NUCLEOTIDE

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (952)

&lt;223&gt; N AT POSITION 952 INDICATES UNDETERMINED NUCLEOTIDE

&lt;400&gt; 53

ctgaaaccat gggcccata cctgctcctg cttatggccc acctgctggc catggccctt 60  
 ggggctgtgg tgcctcaggc cctggaggcc ctcctcagctc gccacccatca ggcccaggcc 120  
 caggctgaac tggctagctt ccaggcagag cacagggcct gcttgcacc tgaggccctg 180  
 gaggagctgc taggtgcggc ctcgtagagca caggccatg gagtttccag cttggcaac 240  
 agctcanaga caagcaactg ggtatctgc tcaatgttgc tgcctactgc cagcatcctc 300  
 accaccacccg gttatggcca catggccca ctctccatcag tggaaaggc cttctgtgtg 360  
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 cttggccctgc acccagccat ttaccacccat gggcagtttgc ctttcttgg ttagtgcctc 720  
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 gccatgggtga aattttttgg gcccagggtgc tctagaaccg atgaagatca agatggccatc 840  
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 accacccctag cctgagccgg aggccaccaag gagttgttgc agaacatagc angaagggtt 960  
 atgggaatga atatgtcatg ggataatgtt aaaaaaaaaa attaaatggg ctgttttagca 1020  
 tgcaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaa 1055

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&lt;210&gt; 54

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (88)

&lt;223&gt; X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

&lt;400&gt; 54

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser  
1 5 10 15Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gly Gln Phe  
20 25 30Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly  
35 40 45Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr  
50 55 60Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
65 70 75 80Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
85 90 95Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
100 105 110Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
115 120 125Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
130 135 140Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
145 150 155 160Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
165 170 175

Leu Gly

&lt;210&gt; 55

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 55

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg  
1 5 10 15Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala  
20 25 30Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln  
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35

40

45

Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
50 55 60

Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
65 70 75 80

His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala  
85 90 95

Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
100 105 110

Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
115 120 125

Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
130 135 140

Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
145 150 155 160

Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
165 170 175

Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg  
180 185 190

Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
195 200 205

Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
210 215 220

Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala  
225 230 235 240

His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr  
245 250 255

Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu  
260 265 270

Thr His Asn Gly Gln Ala Val Gly Leu Gly Gly Leu Ser Cys Leu Ser  
275 280 285

Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala  
290 295 300

Ala Ala Ala Ser Leu  
305

<210> 56  
<211> 304  
<212> PRT  
<213> MUS musculus

<220>  
<221> UNSURE  
<222> (83)  
<223> N AT POSITION 83 INDICATES UNDETERMINED RESIDUE

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&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (198)

&lt;223&gt; N AT POSITION 198 INDICATES UNDETERMINED RESIDUE

&lt;400&gt; 56

Leu Lys Pro Trp Ala Arg Tyr Leu Leu Leu Met Ala His Leu Leu  
1 5 10 15

Ala Met Gly Leu Gly Ala Val Val Leu Gln Ala Leu Glu Gly Pro Pro  
20 25 30

Ala Arg His Leu Gln Ala Gln Val Gln Ala Glu Leu Ala Ser Phe Gln  
35 40 45

Ala Glu His Arg Ala Cys Leu Pro Pro Glu Ala Leu Glu Glu Leu Leu  
50 55 60

Gly Ala Val Leu Arg Ala Gln Ala His Gly Val Ser Ser Leu Gly Asn  
65 70 75 80

Ser Ser Xaa Thr Ser Asn Trp Asp Leu Pro Ser Ala Leu Leu Phe Thr  
85 90 95

Ala Ser Ile Leu Thr Thr Thr Gly Tyr Gly His Met Ala Pro Leu Ser  
100 105 110

Ser Gly Gly Lys Ala Phe Cys Val Val Tyr Ala Ala Leu Gly Leu Pro  
115 120 125

Ala Ser Leu Ala Leu Val Ala Ala Leu Arg His Cys Leu Leu Pro Val  
130 135 140

Phe Ser Arg Pro Gly Asp Trp Val Ala Ile Arg Trp Gln Leu Ala Pro  
145 150 155 160

Ala Gln Ala Ala Leu Leu Gln Ala Ala Gly Leu Gly Leu Leu Val Ala  
165 170 175

Cys Val Phe Met Leu Leu Pro Ala Leu Val Leu Trp Gly Val Gln Gly  
180 185 190

Asp Trp Gln Pro Ala xaa Thr Ile Tyr Phe Cys Phe Gly Ser Leu Ser  
195 200 205

Thr Ile Gly Leu Gly Asp Leu Leu Pro Ala His Gly Arg Gly Leu His  
210 215 220

Pro Ala Ile Tyr His Leu Gly Gln Phe Ala Leu Leu Gly Tyr Leu Leu  
225 230 235 240

Leu Gly Leu Leu Ala Met Leu Leu Ala Val Glu Thr Phe Ser Glu Leu  
245 250 255

Pro Gln Val Arg Ala Met Val Lys Phe Phe Gly Pro Ser Gly Ser Arg  
260 265 270

Thr Asp Glu Asp Gln Asp Gly Ile Leu Gly Gln Asp Glu Leu Ala Leu  
275 280 285

Ser Thr Val Leu Pro Asp Ala Pro Val Leu Gly Pro Thr Thr Pro Ala  
290 295 300

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&lt;210&gt; 57

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)..(9)

&lt;223&gt; X AT POSITIONS 1, 4, AND 5 IS T OR S; X AT POSITION 6 IS I OR V; X AT POSITIONS 2, 3, AND 8 IS Y, F, V, I, M, OR L

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

&lt;400&gt; 57

Xaa Xaa Xaa Xaa Xaa Xaa Gly xaa Gly  
1 5

&lt;210&gt; 58

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)..(8)

&lt;223&gt; X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A, S, OR G; X AT POSITIONS 3, 4, 6, AND 8 ARE M, I, V, L, F, OR Y

&lt;400&gt; 58

Xaa Xaa Xaa Xaa Gly Xaa Pro xaa  
1 5

&lt;210&gt; 59

&lt;211&gt; 7

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: POTASSIUM ION CHANNEL SEQUENCE

&lt;400&gt; 59

Tyr Ala Leu Leu Gly Ile Pro  
1 5

&lt;210&gt; 60

&lt;211&gt; 7

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&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (6)

&lt;223&gt; X AT POSITION 6 IS M, I, V, L, F, OR Y

&lt;400&gt; 60

Tyr Ala Leu Leu Gly Xaa Pro  
1 5

&lt;210&gt; 61

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; UNSURE

&lt;222&gt; (88)

&lt;223&gt; X AT POSITION 88 INDICATES UNDETERMINED RESIDUE

&lt;400&gt; 61

Asn Lys Asn Leu Phe Cys Phe Glu Trp Pro Arg Glu Gly Lys Gly Ser  
1 5 10 15Pro Asp Glu Gln Glu Gln Ser Gln Leu Glu Pro Gly Pro Gln Phe  
20 25 30Lys Ala Thr Arg Gly Gln Pro Ser Ala Glu Gly Ser Ile Gly Val Gly  
35 40 45Arg Asp Pro Ser Arg His Gly Thr Gln Ser Ser His Cys Pro Leu Thr  
50 55 60Leu Ser Ser Pro Gly Tyr Gly His Met Ala Pro Leu Ser Pro Gly Gly  
65 70 75 80Lys Ala Phe Cys Met Val Leu Xaa Ala Leu Gly Leu Pro Ala Ser Leu  
85 90 95Ala Leu Val Ala Thr Leu Arg His Cys Leu Leu Pro Val Leu Ser Arg  
100 105 110Pro Arg Ala Trp Val Ala Val His Trp Gln Leu Ser Pro Ala Arg Ala  
115 120 125Ala Leu Leu Gln Ala Val Ala Leu Gly Leu Leu Val Ala Ser Ser Phe  
130 135 140Val Leu Leu Pro Ala Leu Val Leu Trp Gly Leu Gln Gly Asp Cys Ser  
145 150 155 160Leu Leu Gly Ala Val Tyr Phe Cys Phe Ser Ser Leu Ser Thr Ile Gly  
165 170 175

Leu Gly

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&lt;210&gt; 62

&lt;211&gt; 309

&lt;212&gt; PRT

&lt;213&gt; MUS-musculus

&lt;400&gt; 62

Gly Ile Trp Pro Ser Arg Pro Arg Ile Arg His Glu Glu Asn Val Arg  
1 5 10 15Thr Leu Ala Leu Ile Val Cys Thr Phe Thr Tyr Leu Leu Val Gly Ala  
20 25 30Ala Val Phe Asp Ala Leu Glu Ser Glu Pro Glu Met Ile Glu Arg Gln  
35 40 45Arg Leu Glu Leu Arg Gln Leu Glu Leu Arg Ala Arg Tyr Asn Leu Ser  
50 55 60Glu Gly Gly Tyr Glu Glu Leu Glu Arg Val Val Leu Arg Leu Lys Pro  
65 70 75 80His Lys Ala Gly Val Gln Trp Arg Phe Ala Gly Ser Phe Tyr Phe Ala  
85 90 95Ile Thr Val Ile Thr Thr Ile Gly Tyr Gly His Ala Ala Pro Ser Thr  
100 105 110Asp Gly Gly Lys Val Phe Cys Met Phe Tyr Ala Leu Leu Gly Ile Pro  
115 120 125Leu Thr Leu Val Met Phe Gln Ser Leu Gly Glu Arg Ile Asn Thr Ser  
130 135 140Val Arg Tyr Leu Leu His Arg Ala Lys Arg Gly Leu Gly Met Arg His  
145 150 155 160Ala Glu Val Ser Met Ala Asn Met Val Leu Ile Gly Phe Val Ser Cys  
165 170 175Ile Ser Thr Leu Cys Ile Gly Ala Ala Ala Phe Ser Tyr Tyr Glu Arg  
180 185 190Trp Thr Phe Phe Gln Ala Tyr Tyr Tyr Cys Phe Ile Thr Leu Thr Thr  
195 200 205Ile Gly Phe Gly Asp Tyr Val Ala Leu Gln Lys Asp Gln Ala Leu Gln  
210 215 220Thr Gln Pro Gln Tyr Val Ala Ser Ala Ser Cys Thr Ser Ser Arg Ala  
225 230 235 240His Gly His Arg Arg Phe Leu Asn Leu Val Val Leu Arg Phe Met Thr  
245 250 255Met Asn Ala Glu Asp Glu Lys Arg Asp Ala Glu His Arg Ala Leu Leu  
260 265 270Thr His Asn Gly Gln Ala Val Gly Leu Gly Leu Ser Cys Leu Ser  
275 280 285Gly Ser Leu Gly Asp Gly Val Arg Pro Arg Asp Pro Val Thr Cys Ala  
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290

295

300

Ala Ala Ala Ser Leu  
305

<210> 63  
<211> 434  
<212> PRT  
<213> *Caenorhabditis elegans*

<400> 63  
Met Val Ile Ile Asn Arg Ser Asn Thr Tyr Ala val Glu Gln Glu Ala  
1 5 10 15  
Phe Pro Arg Asp Lys Tyr Asn Ile val Tyr Trp Leu Val Ile Leu Val  
20 25 30  
Gly Phe Gly val Leu Leu Pro Trp Asn Met Phe Ile Thr Ile Ala Pro  
35 40 45  
Glu Tyr Tyr Val Asn Tyr Trp Phe Lys Pro Asp Gly Val Glu Thr Trp  
50 55 60  
Tyr Ser Lys Glu Phe Met Gly Ser Leu Thr Ile Gly Ser Gln Leu Pro  
65 70 75 80  
Asn Ala Ser Ile Asn Val Phe Asn Leu Phe Leu Ile Ile Ala Gly Pro  
85 90 95  
Leu Ile Tyr Arg val Phe Ala Pro Val Cys Phe Asn Ile Val Asn Leu  
100 105 110  
Thr Ile Ile Leu Ile Leu Val Ile Val Leu Glu Pro Thr Glu Asp Ser  
115 120 125  
Met Ser Trp Phe Phe Trp Val Thr Leu Gly Met Ala Thr Ser Ile Asn  
130 135 140  
Phe Ser Asn Gly Leu Tyr Glu Asn Ser Val Tyr Gly val Gly Gly Asp  
145 150 155 160  
Phe Pro His Thr Tyr Ile Gly Ala Leu Leu Ile Gly Asn Asn Ile Cys  
165 170 175  
Gly Leu Leu Ile Thr Val Val Lys Ile Gly Val Thr Tyr Phe Leu Asn  
180 185 190  
Asp Glu Pro Lys Leu Val Ala Ile Val Tyr Phe Gly Ile Ser Leu Val  
195 200 205  
Ile Leu Leu Val Cys Ala Ile Ala Leu Phe Phe Ile Thr Lys Gln Asp  
210 215 220  
Phe Tyr His Tyr His His Gln Lys Gly Met Glu Ile Arg Glu Lys Ala  
225 230 235 240  
Glu Thr Asp Arg Pro Ser Pro Ser Ile Leu Trp Thr Thr Phe Thr Asn  
245 250 255  
Cys Tyr Gly Gln Leu Phe Asn Val Trp Phe Cys Phe Ala Val Thr Leu  
260 265 270

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Thr Ile Phe Pro Val Met Met Thr Val Thr Thr Arg Gly Asp Ser Gly  
275 280 285

Phe Leu Asn Lys Ile Met Ser Glu Asn Asp Glu Ile Tyr Thr Leu Leu  
290 295 300

Thr Ser Phe Leu Val Phe Asn Leu Phe Ala Ala Ile Gly Ser Ile Val  
305 310 315 320

Ala Ser Lys Ile His Trp Pro Thr Pro Arg Tyr Leu Lys Phe Ala Ile  
325 330 335

Ile Leu Arg Ala Leu Phe Ile Pro Phe Phe Phe Cys Asn Tyr Arg  
340 345 350

Val Gln Thr Arg Ala Tyr Pro Val Phe Phe Glu Ser Thr Asp Ile Phe  
355 360 365

Val Ile Gly Gly Ile Ala Met Ser Phe Ser His Gly Tyr Leu Ser Ala  
370 375 380

Leu Ala Met Gly Tyr Thr Pro Asn Val Val Pro Ser His Tyr Ser Arg  
385 390 395 400

Phe Ala Ala Gln Leu Ser Val Cys Thr Leu Met Val Gly Leu Leu Thr  
405 410 415

Gly Gly Leu Trp Pro Val Val Ile Glu His Phe Val Asp Lys Pro Ser  
420 425 430

Ile Leu

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: POTASSIUM ION  
CHANNEL SEQUENCE

<220>

<221> VARIANT

<222> (1)..(7)

<223> X AT POSITION 1 IS Y OR F; X AT POSITION 2 IS A,  
S, OR G; X AT POSITIONS 3, 4, AND 6 ARE M, I, V,  
L, F, OR Y

<400> 64

Xaa Xaa Xaa Xaa Gly Xaa Pro  
1 S

<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus  
sequence between Ce orf1 and Dm orf1

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<400> 65  
Thr Trp Thr Phe  
1

<210> 66  
<211> 4  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence between Ce orf1 and Dm orf1

<400> 66  
Gly Tyr Gly Asn  
1

<210> 67  
<211> 4  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Description of Artificial Sequence: consensus  
sequence between Ce orf1 and Dm orf1

<400> 67  
Gly Phe Gly Asp  
1